S2 Table. Summary of model parameters describing disease progression and choices for the simulations.

Name	Description	Value
$n_{ m E}$	No. of latency Erlang states	16
$n_{ m P}$	No. of prodromal Erlang states	16
$n_{ m I}$	No. of fully contagious Erlang states	16
$n_{ m L}$	No. of late-infectious Erlang states	16
D_E	Average duration of latency period	3.7 days
D_P	Average duration of prodromal period	1 day
D_I	Average duration of fully contagious period	5 days
D_L	Average duration of late infectious period	5 days
ε	Transition rate of latent states	$n_{\rm E}/D_E$
φ	Transition rate of prodromal states	$n_{ m P}/D_P$
γ	Transition rate of early infectious states	$n_{ m I}/D_I$
δ	Transition rate of late-infectious states	$n_{ m L}/D_L$
α	Transition rate from transient multi-infections to multi-infected states	$3.2/\mathrm{day}$
$f_{ m Sick}$	Fraction of symptomatic (sick) infections	58%
$ ilde{f}_{ m Sick}$	Fraction of sympt. multi-infections in fully contagious & late inf. periods	64.4%
$f_{ m Iso}$	Fraction of single-infected (sick) who are isolated (or home isolated)	48%
$ ilde{f}_{ m Iso}$	Fraction of multi-infected (sick) who are isolated (or home isolated)	52.8%
$f_{ m Dead}$	Fraction of single-infected (sick) who die from the disease	4%
$ ilde{f}_{ m Dead}$	Fraction of multi-infected (sick) who die from the disease	5%

Summary of parameters describing the number of Erlang states, durations, transition rates, morbidity and mortality, and their default parameter choices.